

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/196,447DATE: 10/18/2000
TIME: 04:49:03

INPUT SET: S36023.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

ENTERED

(i) APPLICANT: Tripp, Cynthia A.
Frank, Glenn R.
Grieve, Robert B.

(ii) TITLE OF INVENTION: NOVEL PARASITIC HELMINTH
P22U PROTEINS

(iii) NUMBER OF SEQUENCES: 17

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Sheridan Ross P.C.
(B) STREET: 1700 Lincoln St., Suite 3500
(C) CITY: Denver
(D) STATE: CO
(E) COUNTRY: U.S.A.
(F) ZIP: 80203

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/196,447
(B) FILING DATE: 19-NOV-1998
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US/08/460,428A
(B) FILING DATE: 02-JUN-1995

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Connell, Gary J.
(B) REGISTRATION NUMBER: 32,020
(C) REFERENCE/DOCKET NUMBER: 2618-13-3

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 303/863-9700
(B) TELEFAX: 303/863-0223

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47 (2) INFORMATION FOR SEQ ID NO:1:

48

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 913 base pairs

51 (B) TYPE: nucleic acid

52 (C) STRANDEDNESS: single

53 (D) TOPOLOGY: linear

54

55 (ii) MOLECULE TYPE: cDNA

56

57 (ix) FEATURE:

58 (A) NAME/KEY: CDS

59 (B) LOCATION: 3..911

60

61

62 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

63

64 GC GAG TTA AAT AGT CGA ATT TCC GGA GTA CAC CGT AAT ACT GCA GGT 47

65 Glu Leu Asn Ser Arg Ile Ser Gly Val His Arg Asn Thr Ala Gly

66 1 5 10 15

67

68 GCT TTA CAA CGA TTT GCT CTA AAT GGT CAA AAT ACT CTT AAC GAA GGA 95

69 Ala Leu Gln Arg Phe Ala Leu Asn Gly Gln Asn Thr Leu Asn Glu Gly

70 20 25 30

71

72 TCA AGT TAT GAG CCA AAC GGA CTA TTT GTA TTT TCA GCA ATA AAC GGT 143

73 Ser Ser Tyr Glu Pro Asn Gly Leu Phe Val Phe Ser Ala Ile Asn Gly

74 35 40 45

75

76 AGC CAT ACT GAT AGC TTA TCT CAG TAT GGT GAA GGA ATA AAT GAA AAT 191

77 Ser His Thr Asp Ser Leu Ser Gln Tyr Gly Glu Gly Ile Asn Glu Asn

78 50 55 60

79

80 TAT CAT TCT GGA ACT AAT TAT TAT GAT GAA GTA GAA TTA AGA GAT AAA 239

81 Tyr His Ser Gly Thr Asn Tyr Tyr Asp Glu Val Glu Leu Arg Asp Lys

82 65 70 75

83

84 ACA AAT CAG ACA TCG TAC ATT AAT GGA AAT GAT AAT GGA ATC AAT GGA 287

85 Thr Asn Gln Thr Ser Tyr Ile Asn Gly Asn Asp Asn Gly Ile Asn Gly

86 80 85 90 95

87

88 AAG GAT GAT GAA GAT CTG GAT GAA TGC TCT GAT CAA GAA TTC CGA TGT 335

89 Lys Asp Asp Glu Asp Leu Asp Glu Cys Ser Asp Gln Glu Phe Arg Cys

90 100 105 110

91

92 CCA TAT CTA GCT AAA ACA CTT TGT GTT CAT TAT TTG AAA ATA TGC GAT 383

93 Pro Tyr Leu Ala Lys Thr Leu Cys Val His Tyr Leu Lys Ile Cys Asp

94 115 120 125

95

96 GGT ATT GAT GAT TGT GGT GAT GGA AGT GAT GAA ATG AAC TGT GCT GAT 431

97 Gly Ile Asp Asp Cys Gly Asp Gly Ser Asp Glu Met Asn Cys Ala Asp

98 130 135 140

99

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100  GAT GAA GTG ATA ACA TCA ATA AAT GGT AAC GAA TCA ATC AAT ATC AGA      479
101  Asp Glu Val Ile Thr Ser Ile Asn Gly Asn Glu Ser Ile Asn Ile Arg
102      145                      150                      155
103
104  TGT GAT CCG GAT CAA TTT CGA TGT GAA AAT GGA AAA TGT ATC GCA CAA      527
105  Cys Asp Pro Asp Gln Phe Arg Cys Glu Asn Gly Lys Cys Ile Ala Gln
106  160                      165                      170                      175
107
108  ATT GAT CGA TGT AAT CGA AAA TAT GAT TGT GAT GAT GGT ACA GAT GAA      575
109  Ile Asp Arg Cys Asn Arg Lys Tyr Asp Cys Asp Asp Gly Thr Asp Glu
110                      180                      185                      190
111
112  ACA ACT TGT GAA TAT TTC GTG CAA GCT TTG CAA CAA GCG AGA GGT GTA      623
113  Thr Thr Cys Glu Tyr Phe Val Gln Ala Leu Gln Gln Ala Arg Gly Val
114      195                      200                      205
115
116  ACG GTG CAG GAT AAT GCA ATT CGA GAT GAC GAG ATA CCA AAT TAT ACT      671
117  Thr Val Gln Asp Asn Ala Ile Arg Asp Asp Glu Ile Pro Asn Tyr Thr
118      210                      215                      220
119
120  GTA TCC ATG GAA CAG AAA TAC GAT CAA GTA AAG GAA GAT AAG GAG CGG      719
121  Val Ser Met Glu Gln Lys Tyr Asp Gln Val Lys Glu Asp Lys Glu Arg
122      225                      230                      235
123
124  CGA ATG CAA GAG GAG GAG GAA CAG GAA AGG CTG AGA GAG TAC GAG GAA      767
125  Arg Met Gln Glu Glu Glu Glu Gln Glu Arg Leu Arg Glu Tyr Glu Glu
126  240                      245                      250                      255
127
128  CAG ATA CAG GAA AAA TTG AGG CAG GAG GAA GAA AGA GAA CGG CAA GAA      815
129  Gln Ile Gln Glu Lys Leu Arg Gln Glu Glu Glu Arg Glu Arg Gln Glu
130                      260                      265                      270
131
132  CAG GAA AGA AGA CAA AAG GAA CGA GAA AGA ATG GAA CAA GAA AGG ATA      863
133  Gln Glu Arg Arg Gln Lys Glu Arg Glu Arg Met Glu Gln Glu Arg Ile
134      275                      280                      285
135
136  AGA CAA GAA TAT GAT GAA AAG GAA AGA CAA AGG CAA TAT GCT GAA CAG      911
137  Arg Gln Glu Tyr Asp Glu Lys Glu Arg Gln Arg Gln Tyr Ala Glu Gln
138      290                      295                      300
139
140  GC      913
141
142
143  (2) INFORMATION FOR SEQ ID NO:2:
144
145      (i) SEQUENCE CHARACTERISTICS:
146          (A) LENGTH: 303 amino acids
147          (B) TYPE: amino acid
148          (D) TOPOLOGY: linear
149
150      (ii) MOLECULE TYPE: protein
151
152      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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153
154   Glu Leu Asn Ser Arg Ile Ser Gly Val His Arg Asn Thr Ala Gly Ala
155     1           5           10           15
156
157   Leu Gln Arg Phe Ala Leu Asn Gly Gln Asn Thr Leu Asn Glu Gly Ser
158           20           25           30
159
160   Ser Tyr Glu Pro Asn Gly Leu Phe Val Phe Ser Ala Ile Asn Gly Ser
161           35           40           45
162
163   His Thr Asp Ser Leu Ser Gln Tyr Gly Glu Gly Ile Asn Glu Asn Tyr
164           50           55           60
165
166   His Ser Gly Thr Asn Tyr Tyr Asp Glu Val Glu Leu Arg Asp Lys Thr
167           65           70           75           80
168
169   Asn Gln Thr Ser Tyr Ile Asn Gly Asn Asp Asn Gly Ile Asn Gly Lys
170           85           90           95
171
172   Asp Asp Glu Asp Leu Asp Glu Cys Ser Asp Gln Glu Phe Arg Cys Pro
173           100          105          110
174
175   Tyr Leu Ala Lys Thr Leu Cys Val His Tyr Leu Lys Ile Cys Asp Gly
176           115          120          125
177
178   Ile Asp Asp Cys Gly Asp Gly Ser Asp Glu Met Asn Cys Ala Asp Asp
179           130          135          140
180
181   Glu Val Ile Thr Ser Ile Asn Gly Asn Glu Ser Ile Asn Ile Arg Cys
182           145          150          155          160
183
184   Asp Pro Asp Gln Phe Arg Cys Glu Asn Gly Lys Cys Ile Ala Gln Ile
185           165          170          175
186
187   Asp Arg Cys Asn Arg Lys Tyr Asp Cys Asp Asp Gly Thr Asp Glu Thr
188           180          185          190
189
190   Thr Cys Glu Tyr Phe Val Gln Ala Leu Gln Gln Ala Arg Gly Val Thr
191           195          200          205
192
193   Val Gln Asp Asn Ala Ile Arg Asp Asp Glu Ile Pro Asn Tyr Thr Val
194           210          215          220
195
196   Ser Met Glu Gln Lys Tyr Asp Gln Val Lys Glu Asp Lys Glu Arg Arg
197           225          230          235          240
198
199   Met Gln Glu Glu Glu Glu Gln Glu Arg Leu Arg Glu Tyr Glu Glu Gln
200           245          250          255
201
202   Ile Gln Glu Lys Leu Arg Gln Glu Glu Glu Arg Glu Arg Gln Glu Gln
203           260          265          270
204
205   Glu Arg Arg Gln Lys Glu Arg Glu Arg Met Glu Gln Glu Arg Ile Arg

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206                275                280                285
207
208 Gln Glu Tyr Asp Glu Lys Glu Arg Gln Arg Gln Tyr Ala Glu Gln
209      290                295                300
210
211
212 (2) INFORMATION FOR SEQ ID NO:3:
213
214 (i) SEQUENCE CHARACTERISTICS:
215 (A) LENGTH: 1016 base pairs
216 (B) TYPE: nucleic acid
217 (C) STRANDEDNESS: single
218 (D) TOPOLOGY: linear
219
220 (ii) MOLECULE TYPE: cDNA
221
222 (ix) FEATURE:
223 (A) NAME/KEY: CDS
224 (B) LOCATION: 3..626
225
226 (ix) FEATURE:
227 (A) NAME/KEY: 3'UTR
228 (B) LOCATION: 627..1016
229
230
231 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
232
233 GT TTT GTT GTA CTA CTC GTT GTT GCA ATA TGG ATT GAA ATG AGC CAA      47
234 Phe Val Val Leu Leu Val Val Ala Ile Trp Ile Glu Met Ser Gln
235      1                5                10                15
236
237 GGC CAA CAA ATG ATC AAA CAA TGT AAA TGT TCT GAT ATT GCA CCA TGT      95
238 Gly Gln Gln Met Ile Lys Gln Cys Lys Cys Ser Asp Ile Ala Pro Cys
239      20                25                30
240
241 CAA TTA ACT GCC GTT CAA TCA GTT TTA CCA TGT GCT GAT CAA TGC CAG      143
242 Gln Leu Thr Ala Val Gln Ser Val Leu Pro Cys Ala Asp Gln Cys Gln
243      35                40                45
244
245 AAA TAT ATT ACT TCA ATT GGT GGT AAT TAT GAT CAA ATT AGT AAC TGT      191
246 Lys Tyr Ile Thr Ser Ile Gly Gly Asn Tyr Asp Gln Ile Ser Asn Cys
247      50                55                60
248
249 TTT AAA CAG AAA CAA TCA ATT ATA AAT GAT GCT ATG AAA TGT GCT CAA      239
250 Phe Lys Gln Lys Gln Ser Ile Ile Asn Asp Ala Met Lys Cys Ala Gln
251      65                70                75
252
253 GAT GCT TTC CCA AAT GCA TGC GCA CAA GGT GAA CCA AAA ATG GTA CCA      287
254 Asp Ala Phe Pro Asn Ala Cys Ala Gln Gly Glu Pro Lys Met Val Pro
255      80                85                90                95
256
257 AAA CGA TTC GGA AAA GGT CTT CAA TTA GCT GTA ATG ACT GAT ATC AAC      335
258 Lys Arg Phe Gly Lys Gly Leu Gln Leu Ala Val Met Thr Asp Ile Asn

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/196,447

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